

# EMERGING AND REEMERGING HUMAN BUNYAVIRUS INFECTIONS AND CLIMATE CHANGE

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## 26.1 INTRODUCTION

The *Bunyaviridae* family includes a growing number of viruses that have contributed to the burden of emerging and reemerging infectious diseases around the globe. Many of these viruses cause severe clinical outcomes in human and animal populations, the results of which can be detrimental to public health and the economies of affected communities. The threat to endemic and nonnative regions is particularly high, and national and international public health agencies are often on alert. Many of the bunyaviruses cause severe clinical disease including hemorrhage, organ failure, and death leading to their high-risk classification. Hantaviruses and Rift Valley fever virus (RVFV) (genus *Phlebovirus*) are National Institute of Allergy and Infectious Diseases Category A priority pathogens in the United States. Viral hemorrhagic fevers, a classification that includes many bunyaviruses, are immediately notifiable in the European Union. The emergence of new and reemerging bunyaviruses has resulted in numerous human and animal fatalities. Outbreaks of Rift Valley fever (RVF) in East Africa (1997/1998, 2006/2007), Sudan (2007), Southern Africa (2008–2010), Kenya (1997/1998, 2006/2007) (Anyamba et al., 2009, 2010; Breiman et al., 2010; Grobbelaar et al., 2011; Woods et al., 2002) and Saudi Arabia & Yemen (2000, 2010) (Food and Agriculture Organization, 2000; Hjelle and Glass, 2000; Madani et al., 2003) and the emergence of Sin Nombre virus (1993) (Hjelle and Glass, 2000) and most recently Schmallenberg virus (2011) (DEFRA, 2012) are prime examples of the devastating and worldwide toll bunyaviruses have on health and economies.

Climate variability (precipitation and temperature in particular) greatly influence the ecological conditions that drive arboviral disease outbreaks across the globe. Several human and animal disease outbreaks have been influenced by changes in climate associated with the El Niño Southern Oscillation (ENSO) phenomenon including the bunyaviruses RVFV and Sin Nombre (an etiologic agent of hantavirus pulmonary syndrome (HPS)), as well as Murray Valley encephalitis, chikungunya, and malaria to name but a few (Anyamba et al., 2009; Bouma and Dye, 1997; Chretien et al., 2007; Engelthaler et al., 1999; Kovats et al., 2003; Linthicum et al., 1999; Nicholls, 1986). Most bunyaviruses exhibit episodic outbreak patterns with seasonal or annual trends dependent upon climate conditions, vector abundance, and the proximity of a susceptible population. The implications for continued climate change are dire, especially with regard to vector-borne diseases, many of which can cause severe morbidity, sequelae, and death. Increased rainfall and widening endemicity as a result of climate change, compounded by the emergence of new viruses, poses a serious threat to a greater geographic range beyond the regions of endemicity.

## 26.2 BUNYAVIRIDAE FAMILY

Members of the *Bunyaviridae* family are single-stranded RNA viruses with a tripartite genome including a large (L), medium (M), and small (S) RNA segment. Most bunyaviruses are antisense, although some phleboviruses have an ambisense S segment (Baron and Shope, 1996). Virions are enveloped and as such are susceptible to environmental degradation and can be destroyed using lipid solvents, detergents, and low pH solutions. Most bunyaviruses, although not all, are transmitted by arthropods including mosquitoes, ticks,

TABLE 26.1. Bunyaviruses That are Known to Cause Significant Morbidity

Genus	Virus	Primary vector	Affected species	Principle geographic location
<b>Hantavirus</b>	Hantaan	Rodent	Human	Asia
	Puumala	Rodent	Human	Europe
	Seoul	Rodent	Human	Asia, Europe
	Sin Nombre	Rodent	Human	Americas
<b>Nairovirus</b>	CCHF	Tick	Human, bovine, caprine, ovine, cervids	Africa, Asia
	Nairobi sheep disease	Tick	Ovine, human	Africa
<b>Orthobunyavirus</b>	Akabane	Midge, mosquito	Bovine, caprine, ovine	Africa, Asia, Australia
	California encephalitis	Mosquito	Human	North America
	Jamestown Canyon	Mosquito	Human	North America
	La Crosse	Mosquito	Human	North America
<b>Phlebovirus</b>	Schmallenberg	Midge	Ovine, bovine	Europe
	Snowshoe hare	Mosquito	Human	North America
	Naples	Sand fly	Human	Europe, Africa
	Punta Toro	Sand fly	Human	Panama
	RFV	Mosquito	Human, ovine, bovine, caprine, primate, canine, feline, rodent	Africa

midges, and sand flies. Arboviral (arthropod-borne) outbreaks are intimately tied to vector competence, the ecology of which is often a dynamic correlation between climate factors (temperature, rainfall, duration of seasons), reservoir species, and agricultural fecundity. With a broad range of susceptible species, many bunyaviruses are zoonotic and can cause disease in humans as well as many animal species.

Bunyaviruses are especially malignant and pose a threat to numerous animal and human populations across many different continents. While there are many known human, animal, and plant bunyaviruses (a list that grows annually), our discussion herein will be restricted to those that pose a grave threat to human and/or animal life (Table 26.1). The *Bunyaviridae* family poses a serious global threat, one that will continue as new viruses emerge and endemicity expands with the changing climate and globalization.

### 26.2.1 *Hantavirus*

Hantaviruses are found in a diverse number of geographic locations including the Americas, Asia, and Europe, but no clinical cases (only antibody demonstrations) have been reported in Africa or the Middle East (Acha et al., 2003). Each viral species is transmitted by a specific or closely related endemic rodent or insectivore and, as such, is specific to a particular geographic region (Krüger et al., 2011). How the virus is maintained in the wild among susceptible rodents is currently unknown. Native rodents do not show clinical symptoms but do pass virus through excreta that can contaminate the environment and put humans at risk. Virus, while susceptible to dehydration, can remain viable outside the host for many days when protected by moist excreta (Spickler, 2008). Humans acquire infections directly by animal bite or contact with the saliva, feces, or urine of infected animals. Humans can also become infected if they inhale aerosolized virus from these rodent bodily fluids, usually when humans disturb rodent excreta and nests (Acha et al., 2003).

Hantavirus species can cause a wide range of clinical symptoms in humans. While some viral species such as Puumala cause a mild clinical disease, other species can have particularly severe clinical outcomes. Two life-threatening conditions are associated with the hantaviruses: HPS in the Western Hemisphere/New World and hemorrhagic fever with renal syndrome (HFRS) in Asia and Europe (Zhang, 2009).

HPS is a particularly severe manifestation of the many hantaviral diseases. In 1993, a new disease emerged in the Southwestern United States and was initially called “hantavirus pulmonary syndrome” (Acha et al., 2003; Schmaljohn and Hjelle, 1997). It was found to be caused by Sin Nombre virus and spread through the deer mouse (*Peromyscus maniculatus*). The HPS definition still encompasses a narrow clinical spectrum caused by a broad range of viruses within the Hantavirus genus. The initial clinical symptoms of HPS during the first 3–5 days include fever, myalgia, headache, nausea, chills, and dizziness. Patients present with cough and tachypnea progressing to pulmonary edema and hypoxia followed by cardiac abnormalities. With the onset of cardiopulmonary distress, patients decline rapidly requiring hospitalization and ventilation. Even with timely care, HPS has an estimated 40–60% case fatality rate (Acha et al., 2003; Schmaljohn and Hjelle, 1997).

HFRS occurs following infection with, although certainly not limited to, Hantaan virus in Asia and Puumala and Dobrava viruses in Europe. Clinical progression of disease follows five phases: febrile, hypotensive, oliguric, diuretic, and finally convalescent as the kidneys recover function (Acha et al., 2003; Krüger et al., 2011; Schmaljohn and Hjelle, 1997). HFRS patients have abrupt clinical symptoms including fever, chills, prostration, headache, and backache. Additional gastrointestinal symptoms include abdominal pain, nausea, and vomiting. There are also reports of visual impairment/light sensitivity and petechial rash of the trunk or palate. Following the prodromal phase (multiple days to 1 week), proteinuria is observed and renal function declines with subsequent hypotension and oliguria. Most fatalities, as a result of irreversible shock, occur during the hypotensive phase (Schmaljohn and Hjelle, 1997). Hemorrhagic signs include petechiae, hematuria, and melena especially in severe cases. The case fatality rate following HFRS is <0.4% for Puumala virus, 7–12% for Dobrava virus, and 10–15% for Hantaan virus (Acha et al., 2003; Spickler, 2008).

Emerging hantaviruses continue to be identified (Hjelle and Torres-Pérez, 2010). The Hantavirus genus is both genetically and geographically diverse. Numerous genotypes have been identified in both murid and cricetid rodents (the classic reservoir host), while newly identified genotypes with sometimes-unknown pathology have been identified in insectivores (shrews and moles, order *Soricomorpha*) (Kang et al., 2011; Klempa et al., 2007) and bats (order *Chiroptera*) (Hjelle and Torres-Pérez, 2010). There is still much to learn about hantaviruses, but it is clear that they will continue to cause disease in humans around the globe.

### 26.2.2 *Nairovirus*

The *Nairovirus* genus is endemic to diverse geographic ranges that overlap that of its tick vector including Asia, the Middle East, eastern Europe, and Africa (Sang et al., 2011; Zavitsanou et al., 2009). The *Nairovirus* genus is divided into seven serogroups that delineate 37 viruses. Hard ticks of the family *Ixodidae* primarily transmit the nairoviruses. Subsequent exposure to blood, excreta, and tissues of infected humans and animals, in certain serogroups, contributes to secondary infections particularly among caretakers and animal handlers. Many nairoviruses infect animals, but only three are known to cause disease in humans: Crimean–Congo hemorrhagic fever (CCHF), Dugbe, and Nairobi sheep viruses.

Crimean–Congo hemorrhagic fever virus (CCHFV) is naturally maintained in an enzootic cycle between asymptomatic animals and multiple tick species. The most common vectors of CCHFV are from the genus *Hyalomma* (Sang et al., 2011). Many mammalian species have been found to harbor CCHFV including hares and hedgehogs, cattle, sheep, goats, horses, and swine (Acha et al., 2003). Wild animals have been shown to maintain antibody levels against CCHFV including giraffes and rhinos (Spickler, 2009). Birds, while refractory to infection, may play a role in the distribution of infected ticks along migratory routes (Zavitsanou et al., 2009). Small vertebrates, including hares and rodents, amplify the virus and transmit to feeding tick larvae. These ticks maintain the virus throughout their entire life cycle from larvae to adult (transstadial), and in some instances, transovarial, and venereal transmission of virus has occurred; co-feeding transmission has also been implicated (EFSA, 2010). Infected adult ticks, feeding on larger domestic ruminants including cattle, sheep, and goats, pass the virus. Domestic animals remain viremic for 1 week following infection (Spickler, 2009). Humans in close contact with infected ticks, as well as with the infected body fluids expressed during hemorrhage (human), slaughter, and birth, are at greatest risk for disease.

Onset of CCHF is rapid with fever, myalgia, neck pain and stiffness, and photophobia. Gastrointestinal symptoms may be present including nausea, vomiting, and diarrhea. After a few days, patients may become confused or agitated with mood swings followed by a generalized lethargy and depression. CCHF is also accompanied by hemorrhagic conditions including petechiae, ecchymoses, melena, hematuria, and epistaxis. Severe cases end with hepatorenal and pulmonary failure; the case fatality rate is 30% (Acha et al., 2003).

### 26.2.3 *Orthobunyavirus*

The orthobunyaviruses represent a diverse genus of viruses that can result in severe health outcomes including neuroinvasive disease. This genus is divided into 18 distinct serogroups as defined by serologic testing. Of particular importance to humans is the California serogroup that includes La Crosse virus (LCV).

LCV is a zoonotic arboviral disease that circulates between small mammalian hosts (squirrels and chipmunks) and forest-dwelling mosquitoes, *Aedes triseriatus* (Acha et al., 2003). The virus is transmitted both transovarially and sexually in *Aedes*. LCV is most commonly reported in the northern, midwestern, and eastern states of the United States where deciduous forests harbor both host and vector species. Humans are dead-end hosts for LCV. The spectrum of clinical symptoms can be diverse and many individuals develop a subclinical infection. Others experience headache, nausea, vomiting, and fatigue. LCV can result in acute inflammation of the human brain. Severe disease, most often in the pediatric population, can progress to memory loss, seizures, coma, and death (<1%). Neurologic sequelae marked by intellectual deficit and recurring seizures can occur.

New orthobunyaviruses continue to emerge. In late 2011, an unprecedented number of stillbirths with fetal abnormalities were observed in cattle and sheep within Germany and the Netherlands. This new virus, thus far isolated in midges, has been named Schmallenberg virus (DEFRA, 2012; OIE, 2012). Adult cows initially show signs of fever, diarrhea, loss of appetite, and lastly abortion. Offspring of infected animals can be of live birth or stillborn with physical abnormalities including arthrogryposis, ankylosis, or cognitive deficit. The extent of fetal anomaly depends upon the stage of gestation at which infection occurs. Although not known to cause human illness, the economic and agricultural impact of such a virus has been quite serious and the virus continues to spread across the European continent posing problems for trade.

#### 26.2.4 *Phlebovirus*

The *Phlebovirus* genus is comprised of 70 distinct serogroups, of which only a few have been researched in depth and fewer than ten have been linked with disease in humans. Phleboviruses cause a variety of clinical symptoms including self-limiting febrile illness, retinitis, encephalitis, and fatal hemorrhagic fever.

RVF is an economically devastating zoonotic arboviral disease caused by RVFV. Endemic to sub-Saharan Africa, repeated outbreaks have occurred in Kenya, Egypt, Madagascar, and South Africa (Anyamba et al., 2010; Chevalier et al., 2009; Favier et al., 2006; Mohamed et al., 2010; Nguku et al., 2010; Woods et al., 2002). RVFV outbreaks also occur in the Middle East (Balkhy and Memish, 2003; Gerdes, 2004). RVFV is primarily transmitted via mosquitoes, although human contact with infective animal products and aerosolized virus during slaughter and birth can also pose a significant transmission risk (Gerdes, 2004; King et al., 2010; LaBeaud et al., 2011a, b, c; Shope et al., 1982). Sustained RVF outbreaks require a multifaceted convergence of necessary factors: capable vectors, susceptible animals and humans in close proximity, and sufficiently heavy rains. It has been shown that RVFV circulates among endemic animals and humans during interepidemic periods, but only during high-rain seasons are large-scale outbreaks observed (Evans et al., 2008; LaBeaud et al., 2008, 2011a, b, c).

Pregnant domestic livestock are particularly susceptible to severe RVF disease. Human outbreaks of RVFV are often foreshadowed by large “abortion storms” among domestic livestock. The reported rates of abortion in pregnant ewes are 5% to almost 100% and 10–85% in cattle (Spickler, 2006). Young animals also succumb to infection with 90–100% of newborn lambs and 10–70% of calves dying from RVF. Adult animals also die from infection with reported mortality rates among sheep at 5–100% and less than 10% of adult cattle.

Human RVFV infection is typically asymptomatic or, at most, results in a mild to moderate flulike illness with fever, headache, joint pain, and weakness. In a small subset of the population, RVF causes lasting ocular disease (0.5–2%) that contributes to vision loss among affected individuals (Al-Hazmi et al., 2003; LaBeaud et al., 2008, 2011a, b, c). Less than 1% of RVF patients have meningoencephalitis or hemorrhagic fever. Those with meningoencephalitis who survive often suffer long-term neurologic and psychologic sequelae. The case fatality rate following hemorrhagic fever is 50%.

The effect of a RVFV outbreak on an economy is significant, and the impending threat to naïve but susceptible populations is a concern for many governments and producers. The United States alone exported \$8.1 billion beef-related products in 2011. The World Organisation for Animal Health (OIE) imposes a 4-year trade ban on any country with confirmed RVFV transmission, a restriction that is only lifted after 6 months of being disease-free (Linthicum et al., 2007; Little, 2009; World Organization for Animal Health, 2011). Commercial veterinary vaccines, both inactivated and live-attenuated, are available against RVFV in endemic areas of sub-Saharan Africa. There is no commercially available human vaccine.

### 26.3 CLIMATE CHANGE AND *BUNYAVIRIDAE*: CLIMATIC INFLUENCES ON TRANSMISSION CYCLES AND SUBSEQUENT RISK FOR TRANSMISSION OF BUNYAVIRUSES

#### 26.3.1 Arboviral bunyaviruses

**26.3.1.1 Mosquitoes.** Four of the five bunyavirus genera are arthropod-borne. Changes in climate affect disease vectors in a number of ways including mosquito survival;



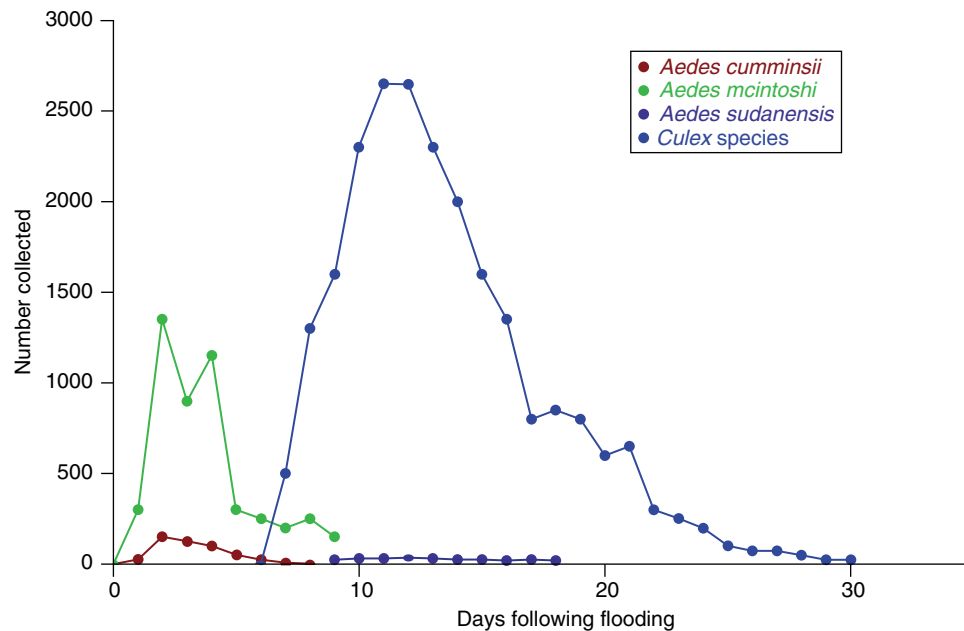
susceptibility to viruses; mosquito population growth rate, distribution, and seasonality; replication and extrinsic incubation period of a virus in the mosquito; and transmission patterns and seasonality (Epstein, 2005; Gubler, 2001). The life cycles of many invertebrates are inextricably linked to temperature, rainfall, and daylight patterns, and any changes herein can have resounding affects on invertebrate vectors.

Mosquito life cycles are particularly susceptible to climatic factors. Taking blood meals is required for the development of eggs, and female mosquitoes will feed repeatedly until repletion (Beaty et al., 1983). High temperatures following complete blood meals quicken the development of eggs within the female mosquito. On average this process lasts between 3 and 4 days (ECDC, 2007; Estrada-Franco et al., 1995). Increases in temperature could both shorten the time necessary for egg development and increase the number of reproductive periods and, subsequently, the absolute number of competent vector offspring produced each season. Mosquito development rates also depend on the ambient temperature. Ideal ranges are between 25 °C and 30 °C, but with consistent temperatures above 25 °C, the developmental time between egg and adult can be as short as 1 week (ECDC, 2007; Estrada-Franco et al., 1995; Turell, 1989; Turell et al., 2001). With regional temperatures on the rise, more eggs can be laid and subsequently more larvae can hatch during each reproductive cycle, thereby creating a much larger population of adult mosquitoes to transmit diseases to susceptible hosts.

East Africa experiences dramatic seasonal rainfall patterns. Cyclic patterns of rainfall and drought contribute greatly to the emergence of arboviral bunyaviruses, and this phenomenon has been observed prior to epizootic RVFV outbreaks in Kenya. *Aedes* mosquitoes lay eggs *above* water lines, a trait that allows for periodic hatching of larvae only during appropriate (sustained wet) conditions. Floodwater *Aedes* species mosquitoes, the vectors of RVFV and LCV, naturally undergo a diapause state to allow survival against environmental extremes including drought and winter. This contributes to vector survival even during long drought periods and has been scientifically shown to aid in the spread of some bunyaviruses including RVFV and LCV (Acha et al., 2003). During short rains, shallow depressions in the landscape fill with water (called *dambos*) and, if sufficient depths are reached, invigorate dormant floodwater *Aedes* mosquito eggs and allow hatching. In the case of RVFV, *Aedes* eggs can be transovarially infected (vertical transmission), thereby replenishing the area with a population of viable and infected mosquitoes, a cycle that can repeat during periods of infrequent rainfall (Mondet et al., 2005). While many African *Aedes* mosquitoes feed on livestock animals, *Culex* mosquitoes primarily provide the bridge between these amplifying domestic livestock and nearby humans, resulting in the epidemic transmission of RVFV. When extreme weather patterns bring excessive rains, much larger bodies of water are formed and provide the ideal environment for reproducing *Aedes* and *Culex* mosquitoes (Figure 26.1).

The conflux of infective *Aedes*, amplifying cattle, and susceptible *Culex* provides the necessary bridge to bring RVFV to humans (Linthicum et al., 1985). RVFV epidemics occur in East Africa every 5–15 years. Epidemics and epizootics are closely linked to the excessive rainfall during ENSO events as sea surface temperatures (SST) warm, not only resulting in a bloom of capable vectors but also providing an ideal environment that places these vectors and susceptible humans in close proximity (Anyamba et al., 2009; Linthicum et al., 1999). Heavy rainfall is often a great relief in drought-ravaged regions, and the growing bodies of water that result cause a mass congregation of people and their animals.

Drought can also impact vector survival. Decreases in rainfall can reduce standing water levels, altering the location and number of small water sources, making ideal habitats for container-breeding mosquitoes.



**Figure 26.1.** Mosquito population succession in a *dambo* habitat (reconstructed after Linthicum et al., 1983). For color detail, please see color plate section.

**26.3.1.2 Ticks.** Like mosquitoes, the successful propagation of ticks is influenced by appropriate weather patterns and the availability of a blood meal. Ticks thrive in warm, humid environments (Süss et al., 2008). Conversely, drought periods increase tick mortality (Githeko et al., 2000). The consequences of climate change are ideal for tick reproduction and success. Increases in global temperatures have the consequence of shortening colder seasons and extending warmer ones, essentially eliminating the seasonal interruption in viral transmission (World Health Organization, 2009). With a warmer winter, tick mortality decreases and the surviving adult ticks can maintain infective levels between seasons. Furthermore, increased numbers of mammalian hosts will survive during temperate winters, providing a plethora of blood meals to feed this increased number of ticks (Githeko et al., 2000).

### 26.3.2 Non-arboviral bunyaviruses

Diseases that do not require a vector for transmission, such as hantaviruses, can also be impacted by climate change as the ecological habitat of rodents is uniquely susceptible to changes in temperature and rainfall. Seasonal weather patterns are often implicated in increases of human hantaviruses (Engelthaler et al., 1999; Hjelle and Glass, 2000; Hjelle and Torres-Pérez, 2010; Jonsson et al., 2010; Schmaljohn and Hjelle, 1997). Outbreaks of Sin Nombre virus in the Southwestern United States are often witnessed when warm winters are followed by wet springs (Calisher et al., 2005a, b). The availability of food (vegetation) for rodents increases in years with the sustained rainfall associated with the ENSO, providing ample food supplies for rodent populations. Reproductive blooms occur during these fertile summer months resulting in ample offspring to replenish the reservoir host pool. Naïve second-generation young adults are susceptible to infection and able to transmit as they



scavenge and fight for food and resources during the subsequent drought period and before the coming winter hibernation season (Calisher et al., 1999; Engelthaler et al., 1999).

While climatic changes do not directly increase viral acquisition or susceptibility of humans per se, these weather patterns do create a “perfect storm” whereby large populations of infected rodents and humans are in closer contact. Public health agencies, in the months and years following ENSO events, have witnessed increases in the number of cases of HFRS (Engelthaler et al., 1999; Hjelle and Glass, 2000; Zhang et al., 2010). Risky behaviors (handling rodent nests and excreta and rodent trappings) are frequently engaged in during the spring months, as people resume their outdoor activities and clean recreational structures (cabins, sheds, etc.) (Jonsson et al., 2010). Disturbing rodent nests and excreta aerosolizes virus that can be inhaled by humans and cause disease.

The linkages that result in increased HFRS cases are complex involving rainfall, vegetation and growth, and complex ecological interactions between reservoirs, prey and predators, and other mammalian species. The role of climate change plays a unique role in the dynamics of each of these parameters and, as such, in disease transmission.

## **26.4 DISEASE SPREAD DUE TO GROWING GEOGRAPHIC DISTRIBUTION OF COMPETENT VECTORS**

### **26.4.1 Physical movement of vectors**

The ENSO phenomenon affects multiple weather conditions including temperature, precipitation, and wind speed and direction. At a local level, these conditions can alter or impede migratory routes for many native bird species, some of which provide blood meals for vector species. Migratory birds can act as a vehicle for disease transmission as they transport infected vector species across and into new regions (Gray et al., 2009).

### **26.4.2 Expansion of suitable range**

The globe is warming. Vertebrates thrive within a specified temperature range and, given slight extensions of temperature on either side of that spectrum, can easily adapt to new bioclimatic conditions. It is important to emphasize that temperature increases can shift the entire range for vector species to a more northerly direction. As global temperatures rise, geographic boundaries expand allowing the successful introduction and subsequent reproduction of nonnative vector species in new territories (Githeko et al., 2000; World Health Organization, 2009). Even after the first generation of vectors die, transovarially transmitted bunyaviruses can remain within the ecosystem. This is not a new phenomenon; many arboviral diseases have spread outside their endemic zones as vectors take up new residence and autochthonous transmission proceeds (Chretien and Linthicum, 2007; Gould and Higgs, 2009).

It has been postulated that the expansion of blue tongue virus (a disease of livestock) has been aided by a warming climate across southern Europe (Purse et al., 2005). Schmallenberg virus, likely transmitted by the same midge vectors, has benefited from the extensive range of these vector species. The broadening geographic range of *Culicoides* midges, as a consequence of this warmer weather, has aided the spread of vector-borne diseases across larger geographic regions (more northward) and for longer periods of time (through the unseasonably warm winter months) (Purse et al., 2005). Additionally, the placement of infective vectors within an area of immunologically naïve hosts increases the risk for human and animal morbidity and continued viral spread.

## 26.5 USING CLIMATE AS A MEANS FOR OUTBREAK PREDICTION

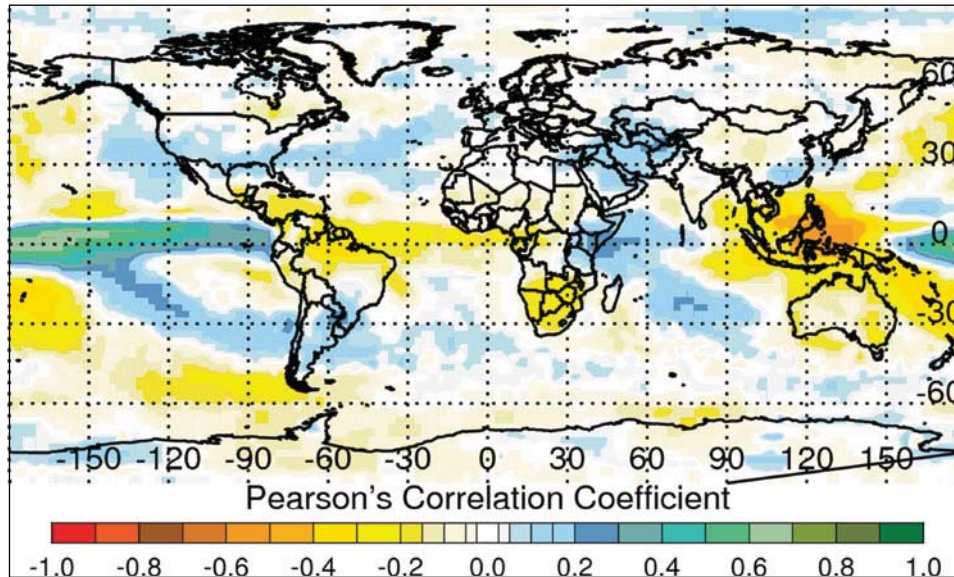
### 26.5.1 Climatic influences

Because bunyaviral outbreaks are linked to weather patterns, researchers can use climate modeling and risk monitoring to predict disease outbreaks, many months in advance, thereby affording public health agencies advanced notification. These methods have been employed to a greater extent in recent years. The benefits of disease prediction are innumerable: the ability for targeted and appropriate implementation of vector control methods, animal vaccinations and trade/movement restrictions, and public education to reduce both human and animal disease. Such an application has been most successful for RVF. Given that the impetus for RVFV outbreaks is often the unusually heavy rainfall associated with local and regional climate variability, the application of climate modeling to RVFV outbreak prediction will be discussed in detail.

Researchers have long observed the association between weather patterns and bunyavirus outbreaks. This is most easily observed during RVFV outbreaks. Davies et al. (1985) reported a composite statistic of surplus rainfall alongside the occurrence of RVFV outbreaks between 1950 and 1982 in Kenya. The four epizootics that occurred during that time were associated with periods of high surplus rainfall (Davies et al., 1985). Studies of outbreaks elsewhere, in South Africa (Swanepoel, 1976, 1981) and West Africa (Bicout and Sabatier, 2004), have additionally supported this relationship. The sustained high precipitation floods *dambos* that support the hatching and continued development of primary and secondary mosquito vectors, increase the likelihood of risky behaviors that place susceptible animals and humans in close proximity to those vectors, and facilitate transmission of RVFV.

The rainfall patterns associated with these outbreaks are inextricably linked to coincident effects of the warm phase of ENSO and warming events in the western equatorial Indian Ocean (increased SST) that result in above-normal and extended rainfall over East Africa (Anyamba and Tucker, 2002; Birkett and Murtugudde, 1999; Cane, 1983; Linthicum et al., 1999; Nicholson, 1986; Ropelewski and Halpert, 1987; Saji et al., 1999). ENSO events are marked by an oscillation between two weather phenomena that have varying effects on the global climate and weather patterns relevant to disease outbreaks. El Niño, the warming ENSO event, refers to a large-scale ocean–atmosphere climate phenomenon that is linked to periodic warming in SST across the Pacific. The opposite ENSO event is La Niña, the cold phase (Figure 26.2). The changes that occur across the sea surface of the Pacific have marked consequences on the temperature and precipitation of tropical climates, especially in the Horn of Africa. El Niño events, or Pacific warming, result in increased rainfall across East Africa, a phenomenon that is largely reversible during cycles of La Niña (Anyamba et al., 2012). More than 90% of RVFV outbreak events since 1950 have occurred during warm ENSO events (Linthicum et al., 1999). The inter-epidemic period of RVFV generally occurs during La Niña events (the cold phase of ENSO), which causes diminished rainfall and drought in East Africa (Anyamba and Tucker, 2002).

Additional ecological parameters conducive to outbreaks have been identified. The vigorous growth of vegetation and cooler temperatures during periods of extended and above-normal rainfall are ecologically appropriate for vector development and propagation and are an additional key to predicting epizootic/epidemic conditions. While *dambos* can be spotted aerially using aircraft-mounted radar and Landsat Thematic Mapper (TM) data, large-scale efforts require high-temporal resolution data so that appropriate pretreatment and vector control efforts can be implemented during high-risk periods (Pope et al., 1994). Such high-temporal resolution data is generated in the form of the normalized difference vegetation index (NDVI) from measurement made by the National Oceanic and Atmospheric Administration (NOAA) series of Polar Operational Environmental Satellites (POES). The



**Figure 26.2.** Correlation of SST and rainfall anomalies illustrates ENSO teleconnection patterns. There is a tendency for above (below)-normal rainfall during *El Niño* (*La Niña*) events over East Africa (Southern Africa, Southeast Asia). Similar differential anomaly patterns were observed for other regions, especially within the global tropics. These extremes (above or below) in rainfall influence regional ecology and consequently dynamics of mosquito disease vector populations and patterns of mosquito-borne disease outbreaks (Anyamba et al., 2012). For color detail, please see color plate section.

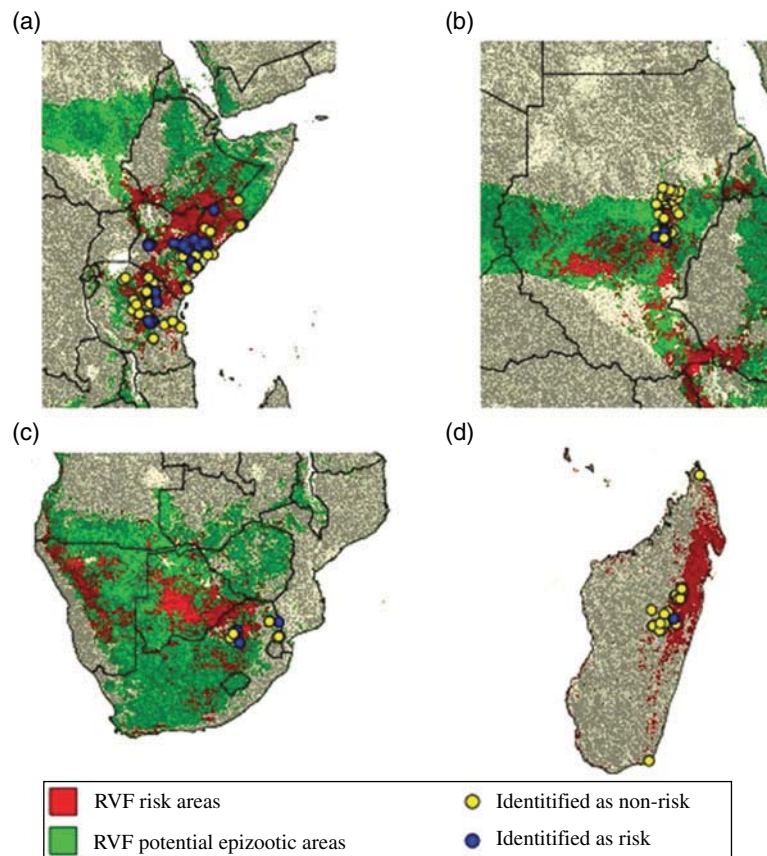
reliability (operational), spatial coverage (global), and temporal frequency (daily) of NOAA satellites has made such data a more cost-effective and successful means of monitoring vegetative habitats conducive to vector development. NDVI data when employed in a time series fashion indicates mosquito habitats (Linthicum et al., 1990, 1987, 1994). These anomalous NDVI changes signal ecological changes conducive to mosquito development and foreshadow the onset of increased RVF cases, allowing for improved prevention and control.

### 26.5.2 Risk mapping and predictions

A monitoring and risk mapping system has been developed that utilizes multiple satellite measurements including SST, outgoing longwave radiation, rainfall, and NDVI-derived landscape data, to assess and predict the climatic and ecological parameters conducive to RVFV outbreaks (Anyamba et al., 2002, 2010; Linthicum et al., 2007). Disease risk mapping and prediction systems take numerous factors into account and have been improved upon as we gain increasingly more sophisticated climatic and ecological data before, during, and after outbreaks. Current systems factor multiple variables including (i) monitoring phase and amplitude anomalies of global SST and western equatorial Indian Ocean SST anomalies within the Niño 3.4 region, (ii) monitoring patterns of outgoing longwave radiation anomalies to infer and detect large scale changes and shift in the major atmospheric centers of tropical convection as resulting from ENSO, and (iii) monitoring anomalous NDVI patterns over Africa as a proxy for ecological dynamics. Historic data also informs risk mapping; epizootic/epidemic regions are mapped and combined with long-term NDVI and rainfall

data to identify areas with high interannual variability to create a potential epizootic area “mask.” The system takes into account anomalous positive NDVI changes that would lead to emergence and propagation of RVF mosquito vectors as shown in Figure 26.1 and pin-points these areas at greater epizootic risk. Using this system to retroactively and prospectively predict RVFV outbreaks has had great success and provides the evidence for valid epizootic/epidemic prediction of other ecologically coupled bunyaviruses in the future.

The developed system operates at near real time and helps to identify ecoclimatic conditions conducive to RVFV outbreaks. Subsequent data provided can be applied to large geographic areas and provides a 3- to 5-month lead time for disease risk (Anyamba et al., 2006, 2010; Linthicum et al., 1999, 2007). This system, as outlined earlier, predicted the RVFV outbreak in Kenya in 2006, 3 months prior to confirmation of disease transmission (Anyamba et al., 2009). These predictions were independently confirmed by entomological and epidemiological field investigations of virus activity in the predicted at-risk region of East Africa (Kenya, Tanzania, Somalia). Subsequent outbreaks in 2007 (Sudan), 2008, 2009, and 2010 (Southern Africa) were predicted using this system (Figure 26.3) (Anyamba et al., 2010; Linthicum et al., 1999). Continued application of this system provides an



**Figure 26.3.** Summary RVF risk map, of Eastern Africa (September, 2006–May, 2007). Areas shown in green represent RVF potential epizootic areas, areas shown in red represent pixels that were mapped by the prediction system to be at risk for RVF activity during the respective time periods, blue dots indicate human cases identified to be in the RVF risk areas, and yellow dots represents human cases in areas not mapped to be at risk. For color detail, please see color plate section.



important tool for the early prevention and control of animal and human diseases at the local, national, and international level.

## 26.6 FUTURE PROBLEMS

The bunyaviruses are of great public health significance because of their geographic diversity and capacity to cause severe disease and death in multiple species. New bunyaviruses will continue to emerge, and known viruses will be found in new regions as favorable conditions expand into new territories. The expansion of endemic ranges threatens human and animal health. Competent vector and reservoir species in the vicinity of susceptible and immunologically naïve humans and animals can maintain newly introduced viruses and cause significant morbidity and mortality. Emerging viruses are identified annually and, as evidenced most recently by Schmallenberg virus, have the propensity to cause significant health and economic consequences. Public health agencies must remain vigilant by reporting unusual clusters of morbidity and mortality. Import and export agencies must also be on high alert and comply with regulations to halt disease spread between endemic and non-endemic regions.

As has been discussed, the geographic range, frequency, and outbreak patterns of bunyaviruses are likely to be influenced by changes in climate. These outbreaks can occur following dramatic and nuanced changes in rainfall, temperature, and wind patterns, the consequences of which have already been observed. Vector-borne diseases and non-arthropod-borne diseases, such as those in the Hantavirus genus, are highly susceptible to climatic variance in a number of ways. Both the proliferation and behaviors of mosquito and tick vectors and reservoir species are largely dependent on abiotic factors in the ecosystem. Changes in weather patterns can lengthen transmission seasons, increase risky behaviors, and shorten extrinsic incubation times. Warning systems used by researchers and government organizations can largely take advantage of this knowledge by using risk mapping and predictions based on known weather phenomena. Continued long-term studies of climate and atmospheric conditions will allow for more advanced predictions in more regions of the globe. With advanced warning, public health officials can unveil targeted vector control, vaccination, and educational campaigns to at-risk communities well in advance of outbreak conditions, thereby thwarting disease spread.

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